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Acting Corporation Counsel

THE CITY OF NEW YORK
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NEW YORK, NEW YORK 10007

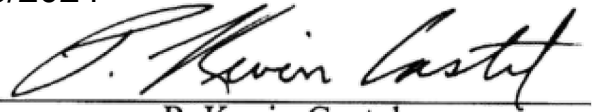
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June 28, 2024

BY ECF

Honorable P. Kevin Castel
United States District Court
Southern District of New York
500 Pearl St. New York, NY 10007-1312

Application provisionally GRANTED.
SO ORDERED.
Dated: 7/3/2024


P. Kevin Castel
United States District Judge

Re: King-Knight v. City of New York, et al.
23-cv-04648 (PKC) (RWL)

Your Honor:

I am a Senior Counsel in the Office of Muriel Goode-Trufant, Acting Corporation Counsel of the City of New York, and the attorney assigned to represent City of New York defendants in the above-captioned matter. [Defendants write to respectfully request permission to file under seal an unredacted copy of Exhibit M to defendants' motion to dismiss, filed today, which consists of two DNA-related reports generated by the Office of the Chief Medical Examiner.] Defendants will file a redacted copy of Exhibit M on the public docket. The redacted copy is attached to this application. Plaintiff consents to this request.

The reason for this request is as follows. New York State Executive Law § 995(d) provides that DNA information may not be disclosed absent consent by the person that is the subject of the DNA analysis, except in criminal cases, or in civil cases where the subject has put his or her own DNA information in issue. Underscoring the state's very strong policy interest in protecting the privacy of DNA information, an intentional violation of this statute is punishable as a felony. *See* New York State Exec. Law § 995(f). Although filing of the unredacted DNA reports would not necessarily violate Section 995(d), in an abundance of caution the City respectfully requests to file an unredacted copy under seal, and file a redacted copy on the public docket in which any specific DNA information is redacted.

We thank the Court for its consideration of this matter

Respectfully submitted,

Alan Scheiner /s/

Alan Scheiner
Senior Counsel
Special Federal Litigation Division

CC: Ugochukwu Uzoh, Esq. (via ECF)
Attorney for Plaintiff

EXHIBIT M



OFFICE OF CHIEF MEDICAL EXAMINER

Department of Forensic Biology
Charles S. Hirsch Center for Forensic Sciences
421 East 26th Street, New York, New York 10016
Official Website: <http://www.nyc.gov/ocme>



Certification of Department of Forensic Biology File as a Business Record

I, Garland Johnson, have been delegated to certify records by Jason K. Graham, M.D., Chief Medical Examiner of the New York City Office of Chief Medical Examiner according to Rule 4518 of the New York Civil Practice Law and Rules.

The Office of Chief Medical Examiner (OCME) is a governmental office organized under §557 of the New York City Charter and Sections 17-201 through 17-206 of the New York City Administrative Code.

All documents and records maintained in the OCME Department of Forensic Biology case file were prepared by the OCME in the regular course of business within the Department of Forensic Biology. It is the regular course of business of the OCME Department of Forensic Biology to prepare the documents and records attached to this certification.

I have examined the original documents and records maintained by the Department of Forensic Biology concerning case file number FB08-05861, and I attest that the documents and records attached to this certification are a true and accurate copy of the original documents and records maintained by the OCME Department of Forensic Biology.

On this 11th day of August 2023, I certify these copies as genuine and as business records of the OCME Department of Forensic Biology.

Garland Johnson

Signature of Name of Certifier



OFFICE OF CHIEF MEDICAL EXAMINER

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Charles S. Hirsch Center for Forensic Sciences
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I have examined the original documents and records maintained by the Department of Forensic Biology concerning case file number: FB08-05861, and I attest that the documents and records attached to this certification are a true and accurate copy of the original documents and records maintained by the OCME Department of Forensic Biology.

On this 19th day of January 2022, I certify these copies as genuine and as business records of the OCME Department of Forensic Biology.

Garland Johnson

Signature of Name of Certifier



MC 1446

FORENSIC BIOLOGY FORM

FORM - Non Conformity Reporting (Type II or III)		
Status: Published		Document ID: 1503
DATE EFFECTIVE 05/02/2017	APPROVED BY Quality Assurance Manager	PAGE 1 OF 3

Instructions: For use on non-conformities discovered during the course of casework. The Principal Investigator must investigate the issue and complete this form. Submit to the Quality Assurance Manager; further action may be required.

Case Number(s) Involved: FB08-05861, FB10-S1042

Date of Occurrence: November 5, 2008

Date of Discovery: November 5, 2021

Description of non-conformity (please be specific):

For the swab taken from the "slide and slide release", the composite profile at [REDACTED] is missing the [REDACTED] allele, and the [REDACTED] allele is missing at [REDACTED] on the case file table. Both alleles repeated in two out of three amplifications at the respective loci.

For the swab taken from the "grips and both front/backstraps", the case file table is missing the [REDACTED] allele at [REDACTED] in rep [REDACTED]. This now has the [REDACTED] allele repeating in two out of three amplifications which changes the composite profile at [REDACTED] to [REDACTED]. Additionally, the [REDACTED] allele is missing from [REDACTED] in rep [REDACTED].

How was this non-conformance identified? (choose one)

Other

If "Other" please provide details: During the 440 motion hearing, the defense expert pointed out the errors on the case file table for the swab taken from the "slide and slide release" during her testimony. While making these corrections, the additional transcriptional errors for the swab taken from the "grips and both front/backstraps" were discovered.

Results of the Root Cause analysis (attach Root Cause worksheets):

The analysis did not correctly transcribe all the alleles from the electropherograms onto the case file table and also did not transcribe all the alleles that repeated at least twice into the composite profile. The tech reviewer also missed these transcriptional errors.

Immediate actions taken to correct the issue (Be specific. Include location of documentation):

An amended case file table was made to include the 2 missing alleles at the respective loci in the composite profile for the swab taken from the "slide and slide release" as well as the 2 missing alleles at the respective loci in rep [REDACTED] for the swab taken from the "grip and both front/backstraps". Also, the composite profile at [REDACTED] for the swab taken from the "grip and both front/backstraps" was updated to include the [REDACTED] allele. This amended case file table was added to both the evidence and suspect files. The overall conclusion with respect to the number

FORENSIC BIOLOGY FORM

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of contributors for the sample (i.e. mixture of at least 3 people) did not change. No additional report will be issued.

Recommended actions taken to correct the Root Cause of the issue (Be specific. Include location of documentation):

The composite profile line was manually entered for ID31 case file tables. However, ID31 is no longer online at the Department of Forensic, and as such, no recommended actions will be given.

Comments: *These typographical errors did not affect any interpretation or reported conclusions, therefore did not have a significant impact to the reported results. KCK 11/30/21*

Principal Investigator (Print): DH

Signature: *DH* Date: 11/18/21

Analyst involved (Print): DH, TAC (*TAC no longer works at OCME - KCK 11/22/21*)

Signature: *DH* Date: 11/30/21

Immediate Supervisor, if applicable (Print): EL

Signature: *[Signature]* Date: 11/30/21

Review by QA Manager:

- ☒ No additional information/corrections required
- ☒ Form **does not** need to be forwarded to the OCME Root Cause Analysis Officer
- ☐ Additional information/corrections **required**
- ☐ Form **has been** forwarded to the OCME Root Cause Analysis Officer

FB08-05861

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FORM - Non Conformity Reporting (Type II or III)		
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Comments:

Signature: Kyo McElroy Date: 11/22/21
11/22/21

FB08-05861

Controlled versions of Department of Forensic Biology Manuals only exist in the Forensic Biology Qualtrax software. All printed versions are non-controlled copies.

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OFFICE OF CHIEF MEDICAL EXAMINER
520 First Avenue, New York, New York 10016

DEPARTMENT OF FORENSIC BIOLOGY
421 East 26th Street, New York, New York 10016
Mechthild Prinz, PhD, Director
Telephone: 212.323.1200 Fax: 212.323.1590
Email: dnalab@ocme.nyc.gov
Official Website: <http://www.nyc.gov/ocme>



DATE: December 14, 2010

LABORATORY REPORT

VICTIM: [REDACTED]

LAB NO: FB08-05861

COMPLAINT NO: 2008-046-11016

START DATE: 12/14/10

ADDITIONAL REPORT

This is an additional report. For previous results, evidence received, and disposition, see report dated November 5, 2008.

RESULTS AND CONCLUSIONS:

The combined probability of inclusion was calculated for the sample listed below:

- swab taken from the "slide and slide release"

The combined probability of inclusion, that is, the probability that a random individual would be included as a possible contributor to this mixture of labeled DNA alleles, is:

15 loci result (swab from "slide and slide release")
1 in 27.9 people

Analyst: _____

Diana Ho

Diana Ho
Criminalist III

Administrative Review Date: 12/30/10

Administrative Reviewer: _____

Jaheida Perez

APPENDIX

Identification of Blood, Semen and Saliva:

The finding of human blood is based on a positive screening test for blood followed by the detection of human (primate) DNA. **Blood presumptively found** is based on a positive screening test for blood.

Semen has two components: the seminal plasma (which contains a protein called P30) and spermatozoa. Semen can be identified by detecting P30 and/or sperm.

The detection of an elevated level of **amylase** indicates, but does not conclusively establish, the presence of saliva. Sources of amylase may include (but are not limited to) saliva, vaginal secretions, and bacteria.

Background to DNA Testing

DNA (Deoxyribo-Nucleic Acid), the inherited genetic material found in cells, contains markers which can differ from person to person. **DNA testing** can determine these genetic markers and compare biological samples from different individuals.

Alternative forms of DNA markers are called **alleles**. Alleles are found at specific areas, or locations, of the DNA called **loci** (singular, **locus**).

STR (short tandem repeat) loci contain alleles with a variable number of short repeating segments. Each STR allele can be described using a number which represents its number of repeats. A **DNA profile** is the series of numbers describing the DNA alleles found at an individual's STR DNA loci.

DNA Testing

DNA testing involves several steps, including DNA extraction, DNA quantitation, PCR/DNA amplification, and analysis of the resulting DNA alleles.

DNA extraction recovers DNA from biological samples such as blood, bone, hair, saliva, semen, and skin cells.

Differential extraction is designed to physically separate the DNA in epithelial cells from the DNA in sperm cells, in samples which potentially contain a mixture of sperm and other cell types. As a result, separate "epithelial cell," "sperm cell," and "swab (or substrate) remains" DNA fractions are generated. Incomplete separation can occur and fractions may contain both sperm DNA and epithelial cell DNA.

DNA quantitation measures the amount of DNA extracted from samples by using a technique called quantitative real time polymerase chain reaction (qRT-PCR). If sufficient DNA is detected, DNA amplification and analysis can be attempted.

The **PCR** (polymerase chain reaction) technique produces large amounts of DNA from small starting amounts of DNA by repeated cycles of copying the DNA loci (**DNA amplification**); after amplification the alleles present in the sample are identified.

PCR DNA testing for STRs uses the **Applied Biosystems AmpFISTR Identifier® PCR Amplification Kit** with 28 amplification cycles (**Identifier® 28**) or 31 amplification cycles (**Identifier® 31**). Each STR locus tested in the Identifier® Kit contains between 8 and 32 identifiable alleles. The **Applied Biosystems AmpFISTR Minifiler™ PCR Amplification Kit** may also be used. These Kits also test the Amelogenin locus, which is used to determine the sex origin of a sample.

High sensitivity PCR DNA testing uses Identifier® 31 and replicate PCR tests when very low amounts of DNA (< 20 pg/μL) are present in a sample or when Identifier® 28 testing does not yield an adequate DNA profile.

FB08-05861

Colleen Shepherd

Y- chromosome STRs (Y-STR) are male-specific STRs, not present in females, that are inherited from father to son, and should be identical for all male relatives of the paternal line. For example, brothers who share the same father will have the same Y-STR type. PCR DNA testing for Y-STRs uses the **Promega PowerPlex® Y STR Kit** with 30 cycles.

Statistics:

The rarity of a DNA profile can be expressed as an **STR population frequency estimate**, how often one would expect to see the DNA profile. STR population frequency estimates are based on the OCME STR database, the Population Data in the AmpF/STR® Identifier™ PCR Amplification Kit User's Manual (2001) Population Data, Applied Biosystems, Foster City, California, the US YSTR Database, National Center for Forensic Science, Orlando, FL, the DNA View Program, Brenner, CH (1997) Symbolic Kinship program, Genetics 145:535-542, and the National Research Council (1996) The Evaluation of Forensic DNA Evidence, Natl. Acad. Press, Washington DC.

The statistical values reported reflect the approximate frequency of occurrence of a DNA profile in a population of unrelated individuals. Therefore, these are not appropriate for relatives. A profile is considered unique if it is at least as rare as 1 in greater than 6.80 trillion unrelated people.

Conclusions for DNA Typing

Is the source of: The DNA profile of an individual matches an evidentiary DNA profile and the population frequency of the evidentiary DNA profile meets the threshold of 1 in greater than 6.80 trillion, assuming the source is not an identical twin.

Could be the source of: The DNA profile of an individual is consistent with an evidentiary DNA profile, and the population frequency of the evidentiary DNA profile does not meet the threshold of 1 in greater than 6.80 trillion unrelated people.

Is a major or minor contributor to the mixture: The DNA profile of an individual matches a major or minor evidentiary DNA profile determined from a mixture, and the DNA population frequency of the determined major or the minor DNA profile meets the threshold of 1 in greater than 6.80 trillion individuals, assuming that source is not an identical twin.

Could be a major or minor contributor to the mixture: The DNA profile of an individual is consistent with a major or minor evidentiary DNA profile determined from a mixture, and the DNA population frequency of the determined major or the minor DNA profile does not meet the threshold of 1 in greater than 6.80 trillion unrelated people.

Could be a contributor to the mixture: For mixtures where individual profiles were not determined, all of the DNA alleles seen in an individual's DNA profile were also seen in the mixture for the locations where comparisons could be made.

Cannot be excluded as a contributor to the mixture: For the locations where comparisons could be made, most of the DNA alleles seen in an individual's DNA profile were also seen in the mixture. The allele(s) that were absent could be explained by any of several factors. Therefore, this person cannot be ruled out as a possible contributor to the mixture.

Excluded as a contributor to the mixture: For the locations where comparisons could be made, one or more of the DNA alleles seen in an individual's DNA profile were not seen in the mixture and this absence cannot be explained. Therefore, this person can be ruled out as a contributor.

No conclusions can be drawn: For the locations where comparisons could be made, the results do not support a positive association or an exclusion. Therefore, it cannot be determined whether a person contributed to this mixture.

Not suitable for comparison: The DNA results on the evidence are either too incomplete or too complex to be the basis for conclusions regarding the source of the DNA.